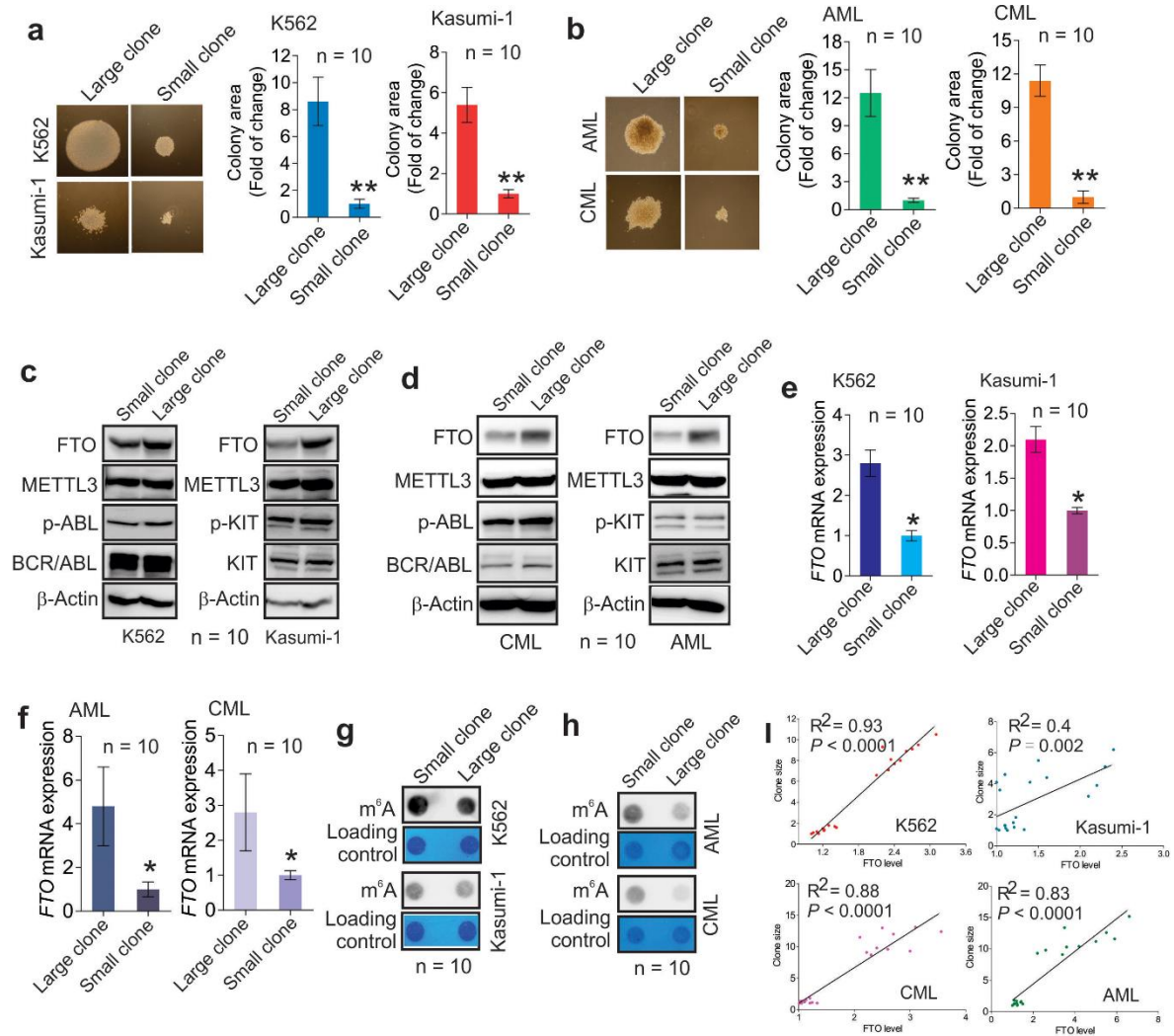


**Figure S5**



**Figure S5.** The FTO-m<sup>6</sup>A axis reflects the heterogeneous nature of leukemia cell populations. The leukemia cell lines (K562, Kasumi-1) and patient primary cells (CML, AML) were subjected to colony-forming assays and the single colonies (n = 10/cell type/group) were selected for further investigations. **a,b** Left, representative images of colonies; graph is the quantification of colony sizes. **c,d** The protein lysates of 10 colonies were pooled and subjected to Western blotting. **e,f** qPCR for *FTO* expression in large and small colonies. **g,h** The mRNA from 10 colonies were pooled and subjected to dotblotting. Data are mean  $\pm$ SD; \**p* < 0.05, \*\**p* < 0.01. **i** Scatter plot

showing the correlation of *FTO* expression and colony sizes reported in (a) and (b). R: Pearson correlation coefficients;  $R^2$ : means ‘the goodness of fit’. Statistical significance was calculated by Pearson correlation coefficients.